

OIPE

P#9

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/497,967

DATE: 08/15/2001

TIME: 09:27:50

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Output Set: N:\CRF3\08132001\I497967.raw

3 <110> APPLICANT: Clark, Theodore G.
 4 Dickerson, Jr., Harry W.
 5 Lin, Tian-Long
 7 <120> TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
 8 ICHTHYOPHTHIRIUS
 10 <130> FILE REFERENCE: 235.00170101
 12 <140> CURRENT APPLICATION NUMBER: 09/497,967
 13 <141> CURRENT FILING DATE: 2000-02-04
 15 <150> PRIOR APPLICATION NUMBER: 60/131,121
 16 <151> PRIOR FILING DATE: 1999-04-27
 18 <150> PRIOR APPLICATION NUMBER: 60/118,634
 19 <151> PRIOR FILING DATE: 1999-02-04
 21 <150> PRIOR APPLICATION NUMBER: 60/122,372
 22 <151> PRIOR FILING DATE: 1999-03-02
 24 <150> PRIOR APPLICATION NUMBER: 60/124,905
 25 <151> PRIOR FILING DATE: 1999-03-17
 27 <160> NUMBER OF SEQ ID NOS: 102
 29 <170> SOFTWARE: PatentIn Ver. 2.1
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1326
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Ichthyophthirius multifiliis
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 39 cttggtactt gtgttaattg cagacctaat ttttactata atgggtggtgc tgcttaagga 180
 40 gaagctaatt gtaattaacc tttcgcagca aataatgctg cttagaggtat atgtgtacca 240
 41 tgccaaataa acagagtagg ctctgttacc aatgcagggtg acttagctac ttttagccaca 300
 42 taatgcagta cttaatgtcc tactggcact gcacttgatg atggagtgc agatgttttt 360
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 50 ataaacaaaa acgattctcc tgccactgca ggtgcctaag ctaatttagc cacataatgc 840
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 52 tcatccacat aatgttctta atgcattgct aattactttt ttaatggtaa tttcgaagca 960
 53 ggtaaaagtt aatgttttaa gtgtccagta agtaaaacta ctccagcaca tgctccagggt 1020
 54 aatactgcta cttaagccac ataatgtttg accacatgtc ctgctggtac agtacttgat 1080
 55 gatggaacat caactaattt tgtagcttcc gcaactgaat gtactaaatg ttctgctggc 1140
 56 ttttttgcac caaaaacaac tggttttaca gcagggtactg atacatgtac tgaatgtact 1200
 57 aaaaaattaa cttctggtgc cacagctaaa gtatatgctg aagctactca aaaagtataa 1260
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 62 <210> SEQ ID NO: 2

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p. 5

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63 <211> LENGTH: 2486

64 <212> TYPE: DNA

65 <213> ORGANISM: Ichthyophthirius multifiliis

67 <400> SEQUENCE: 2

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70 tttaaaaaatt atttatgatt tgtttttaga aaataagggt ttatttataa taatgaattc 180
71 ttaaaaataat gaatcgatat tatataaatt tttatttttt ataaaaatatt gaattaccta 240
72 aaataatata aatttatgaa atattattta aaataataag ttatagaata aattttattt 300
73 tttttctaatt tttttttata attattaaaa aaaaaaaaaa aatctattac tttttgcat 360
74 ttacaaacga tagaaaaaac taaaatttat aatattatta aaaaaaaaaa tataaataat 420
75 aataataaaa atatgaaata taatatttta ttaattttaa ttatttcttt atttattaat 480
76 gaattaagag ctgttccatg tcctgatggg acttagactc aagctggatt gactgatgta 540
77 ggtgctgctg atcttggtac ttgtgttaat tgcagaccta atttttacta taatgggtgg 600
78 gctgcttaag gagaagctaa tggttaattaa ctttcgcag caaataatgc tgctagaggt 660
79 atatgtgtac catgccaaat aaacagagta ggctctgtta ccaatgcagg tgacttagct 720
80 acttttagcca cataatgcag tacttaatgt cctactggca ctgcacttga tgatggagtg 780
81 acagatgttt ttgatagatc agccgcataa tgtgttaaat gcaaacctaa cttttactat 840
82 aatgggtggt ctcttaagg tgaagctcct ggctttaag tttttgctgc tgggtgctgcc 900
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84 tctcctgcc ctgcagggtgc ctaagctaatt ttagccacat aatgtagcaa ttaatgtcct 1020
85 actggcactg tacttgatga tggagtga caa cttgttttta atacatcagc cacattatgt 1080
86 gttaaatgca gacctaactt ttactataat ggtggttctc cttaagggtga agtcctggc 1140
87 gtttaagttt ttgctgctgg tgctgcccgt gcagggtgtg ctgccgttac tagttaatgt 1200
88 gtaccttgcc aaataaacia aaacgattct cctgccactg cagggtgccta agctaattta 1260
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93 acagtacttg atgatggaac atcaactaat tttgtagctt ccgcaactga atgtactaaa 1560
94 tgttctgctg gcttttttgc atcaaaaaca actgggttta cagcaggtag tgatacatgt 1620
95 actgaatgta ctaaaaaatt aacttctggt gccacagcta aagtatatgc tgaagctact 1680
96 caaaaagtat aatgcgcctc cactactttc gctaaatttt tatcgatttc cttattattt 1740
97 atttctttct atttattgtg atgaataaaa taattcatat tattttattt ttttatttta 1800
98 tgtttataaa ttaaaaaata gataaaattt aaaatatatt aaaaataatt ttttatataa 1860
99 attatcaatt aacaactaac taacaaaata caattaaaat ctttatagaa ggtttttctt 1920
100 tataatattt taaggattaa tttacaaatt ttaattaaag taacatttta tcatttaaaa 1980
101 tcttatttaa ataaatacat aaattctagt tgattctttt ttaatatata tttaaaatta 2040
102 gaataaaaaa atatgtttta agtaaaaaa agaagaaatt taatttaatt ttttatatt 2100
103 taattttaata tttatttaatt ttattttcga atattttatt atcaaacttt taaaactaaa 2160
104 aatttattaa gtctaattta aactatatat atttatattt tttgtattct tttttttatt 2220
105 cataatcata aatacagaat tttttatatt ttgagttgtg catattattt tatgaatgtt 2280
106 atcacttata tatgcgtatg taattttatt tatctattc agggcttaag cttgtaaaat 2340
107 aataatattc aatatatttg ttaagggaaa ggtaggcaa actaaactaa attttttaac 2400
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109 atttatttat aacactaaaa gaattc 2486
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 1404
114 <212> TYPE: DNA

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115 <213> ORGANISM: Ichthyophthirius multifiliis

117 <400> SEQUENCE: 3

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120 cctgcaaatt gtgttaattg ttagaaaaac ttttattata ataatgctgc tgctttcgtt 180
121 cctggtgcta gtacgtgtac acctgtcca taaaaaaaag atgctggtgc ttaaccaaatt 240
122 ccacctgcta ctgctaattt agtcacataa tgtaacgtta aatgccctgc tggtagcgca 300
123 attgcagggtg gagcaacaga ttatgcagca ataatcacag aatgtgttaa ttgtagaatt 360
124 aattttttata atgaaaatgc tccaaatttt aatgcagggtg ctagtacatg cacagcttgt 420
125 ccggtaaaca gagttggtgg tgcattgact gctggtaatg ccgctaccat agtcgcataa 480
126 tgtaacgtcg catgtcctac tggtagtga cttgatgatg gagtaactac tgattatgtt 540
127 agatcattca cagaatgtgt taaatgtaga cttaactttt actataatgg taataatggg 600
128 aatactcctt tcaatccagg taaaagttaa tgcacacctt gtccggcaat taaacctgct 660
129 aatgttgctt aagctacttt aggtaatgat gctacaataa ccgcataatg taacgttgca 720
130 tgccctgatg gtactataag tgctgctgga gtaaataatt gggtagcaca aaacactgaa 780
131 tgtactaatt gtgctcctaa cttttacaat aataatgctc ctaatttcaa tccaggtaat 840
132 agtacatgcc taccttgccc agcaaataaa gattatggtg ctgaagccac tgcagggtgg 900
133 gccgctactt tagccaaata atgtaatat gcatgccctg atggtactgc aattgctagt 960
134 ggagcaacta attatgtaat attataaaca gaatgtctaa attgtgctgc taacttttat 1020
135 tttgatggta ataatttcta ggcagggaag agtagatgca aagcatgtcc agcaaataaa 1080
136 gtttaaggcg ctgtagcaac tgcagggtgt actgctactt taaatgcata atgtgccctt 1140
137 gaatgccctg ctggtactgt actcaccgat ggaacaacat ctacttataa ataagcagca 1200
138 tctgaatgtg ttaaatgtgc tgccaacttt tatactacaa aataaactga ttgggtagca 1260
139 ggtattgata catgtactag ttgtaataaa aaattaactt ctggcgctga agctaattta 1320
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144 <210> SEQ ID NO: 4

145 <211> LENGTH: 100

146 <212> TYPE: DNA

147 <213> ORGANISM: Ichthyophthirius multifiliis

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154 <210> SEQ ID NO: 5

155 <211> LENGTH: 1404

156 <212> TYPE: DNA

157 <213> ORGANISM: Artificial Sequence

159 <220> FEATURE:

160 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic

161 55kD i-antigen coding region

163 <400> SEQUENCE: 5

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166 cctgctaact gtgtgaactg tcagaagaac ttctactaca acaacgctgc tgctttcgtg 180
167 cctggagctt ctacctgtac cccttgctct cagaagaagg acgctggagc tcagcctaac 240
168 cctcctgcta ccgctaacct ggtgacctag tgtaacgtga agtgcctgc tgggaaccgct 300
169 atcgctggag gagctaccga ctacgctgct atcatcaccg agtgtgtgaa ctgtcgcatc 360
170 aacttctaca acgagaacgc tcctaacttc aacgctggag cttctacctg taccgcttgt 420
171 cctgtgaacc gcgtgggagg agctctgacc gctggaaacg ctgctaccat cgtggctcag 480

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172 tghtaacgtgg cttgtcctac cggaaccgct ctggacgacg gactgaccac cgactacgtg 540
173 cgctctttca ccgagtgtgt gaagtgtcgc ctgaacttct actacaacgg aaacaacgga 600
174 aacacccctt tcaaccctgg aaagtctcag tgtacccctt gtcctgctat caagcctgct 660
175 aacgtggctc aggtaccctt gggaaacgac gctaccatca ccgctcagtg taacgtggct 720
176 tgtcctgacg gaaccatctc tgctgtctgga gtgaacaact ggggtggctca gaacaccgag 780
177 tgtaccaact gtgtccttaa cttctacaac aacaacgctc ctaacttcaa ccctggaaac 840
178 tctacctgtc tgccttgctc tgctaacaag gactacggag ctgaggctac cgctggagga 900
179 gctgctaccc tggctaagca gtgtaacatc gcttgctctg acggaaccgc tatcgcttct 960
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182 gtgcaggag ctgtggctac cgctggagga accgctaccc tgatcgctca gtgtgctctg 1140
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184 tctgagtgtg tgaagtgtgc tgctaacttc tacaccacca agcagaccga ctgggtggct 1260
185 ggaatcgaca cctgtacctc ttgtaacaag aagctgacct ctggagctga ggctaacctg 1320
186 cctgagtctg ctaagaagaa catccagtgt gacttcgcta acttctctgtc tatctctctg 1380
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191 <211> LENGTH: 442
192 <212> TYPE: PRT
193 <213> ORGANISM: Ichthyophthirius multifiliis
195 <400> SEQUENCE: 6
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197 1 5 10 15
199 Glu Leu Arg Ala Val Pro Cys Pro Asp Gly Thr Gln Thr Gln Ala Gly
200 20 25 30
202 Leu Thr Asp Val Gly Ala Ala Asp Leu Gly Thr Cys Val Asn Cys Arg
203 35 40 45
205 Pro Asn Phe Tyr Tyr Asn Gly Gly Ala Ala Gln Gly Glu Ala Asn Gly
206 50 55 60
208 Asn Gln Pro Phe Ala Ala Asn Asn Ala Ala Arg Gly Ile Cys Val Pro
209 65 70 75 80
211 Cys Gln Ile Asn Arg Val Gly Ser Val Thr Asn Ala Gly Asp Leu Ala
212 85 90 95
214 Thr Leu Ala Thr Gln Cys Ser Thr Gln Cys Pro Thr Gly Thr Ala Leu
215 100 105 110
217 Asp Asp Gly Val Thr Asp Val Phe Asp Arg Ser Ala Ala Gln Cys Val
218 115 120 125
220 Lys Cys Lys Pro Asn Phe Tyr Tyr Asn Gly Gly Ser Pro Gln Gly Glu
221 130 135 140
223 Ala Pro Gly Val Gln Val Phe Ala Ala Gly Ala Ala Ala Ala Gly Val
224 145 150 155 160
226 Ala Ala Val Thr Ser Gln Cys Val Pro Cys Gln Leu Asn Lys Asn Asp
227 165 170 175
229 Ser Pro Ala Thr Ala Gly Ala Gln Ala Asn Leu Ala Thr Gln Cys Ser
230 180 185 190
232 Asn Gln Cys Pro Thr Gly Thr Val Leu Asp Asp Gly Val Thr Leu Val
233 195 200 205
235 Phe Asn Thr Ser Ala Thr Leu Cys Val Lys Cys Arg Pro Asn Phe Tyr
236 210 215 220

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238 Tyr Asn Gly Gly Ser Pro Gln Gly Glu Ala Pro Gly Val Gln Val Phe
239 225      230      235      240
241 Ala Ala Gly Ala Ala Ala Ala Gly Val Ala Ala Val Thr Ser Gln Cys
242      245      250      255
244 Val Pro Cys Gln Ile Asn Lys Asn Asp Ser Pro Ala Thr Ala Gly Ala
245      260      265      270
247 Gln Ala Asn Leu Ala Thr Gln Cys Ser Thr Gln Cys Pro Thr Gly Thr
248      275      280      285
250 Ala Ile Gln Asp Gly Val Thr Leu Val Phe Ser Asn Ser Ser Thr Gln
251      290      295      300
253 Cys Ser Gln Cys Ile Ala Asn Tyr Phe Phe Asn Gly Asn Phe Glu Ala
254 305      310      315      320
256 Gly Lys Ser Gln Cys Leu Lys Cys Pro Val Ser Lys Thr Thr Pro Ala
257      325      330      335
259 His Ala Pro Gly Asn Thr Ala Thr Gln Ala Thr Gln Cys Leu Thr Thr
260      340      345      350
262 Cys Pro Ala Gly Thr Val Leu Asp Asp Gly Thr Ser Thr Asn Phe Val
263      355      360      365
265 Ala Ser Ala Thr Glu Cys Thr Lys Cys Ser Ala Gly Phe Phe Ala Ser
266      370      375      380
268 Lys Thr Thr Gly Phe Thr Ala Gly Thr Asp Thr Cys Thr Glu Cys Thr
269 385      390      395      400
271 Lys Lys Leu Thr Ser Gly Ala Thr Ala Lys Val Tyr Ala Glu Ala Thr
272      405      410      415
274 Gln Lys Val Gln Cys Ala Ser Thr Thr Phe Ala Lys Phe Leu Ser Ile
275      420      425      430
277 Ser Leu Leu Phe Ile Ser Phe Tyr Leu Leu
278      435      440
281 <210> SEQ ID NO: 7
282 <211> LENGTH: 468
283 <212> TYPE: PRT
284 <213> ORGANISM: Ichthyophthirius multifiliis
286 <400> SEQUENCE: 7
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291      20      25      30
293 Gly Gln Val Asp Asp Leu Gly Thr Pro Ala Asn Cys Val Asn Cys Gln
294      35      40      45
296 Lys Asn Phe Tyr Tyr Asn Asn Ala Ala Ala Phe Val Pro Gly Ala Ser
297      50      55      60
299 Thr Cys Thr Pro Cys Pro Gln Lys Lys Asp Ala Gly Ala Gln Pro Asn
300 65      70      75      80
302 Pro Pro Ala Thr Ala Asn Leu Val Thr Gln Cys Asn Val Lys Cys Pro
303      85      90      95
305 Ala Gly Thr Ala Ile Ala Gly Gly Ala Thr Asp Tyr Ala Ala Ile Ile
306      100      105      110
308 Thr Glu Cys Val Asn Cys Arg Ile Asn Phe Tyr Asn Glu Asn Ala Pro
309      115      120      125

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VERIFICATION SUMMARY

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L:735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
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L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
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